

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/718,359

Source: 1FWO

Date Processed by STIC: 1/12/05

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IFWO

RAW SEQUENCE LISTING

DATE: 01/12/2005

PATENT APPLICATION: US/10/718,359

TIME: 11:34:06

Input Set : A:\041116.US 275.00080101.ST25.txt

Output Set: N:\CRF4\01122005\J718359.raw

3 <110> APPLICANT: MEDICAL COLLEGE OF GEORGIA RESEARCH INSTITUTE, INC.
 5 <120> TITLE OF INVENTION: NaCT AS A TARGET FOR LIFESPAN EXPANSION AND WEIGHT REDUCTION
 7 <130> FILE REFERENCE: 275.0008 0101
 9 <140> CURRENT APPLICATION NUMBER: 10/718,359
 10 <141> CURRENT FILING DATE: 2003-11-20
 12 <150> PRIOR APPLICATION NUMBER: 60/428,469
 13 <151> PRIOR FILING DATE: 2002-11-22
 15 <150> PRIOR APPLICATION NUMBER: 60/459,441
 16 <151> PRIOR FILING DATE: 2003-04-01
 18 <160> NUMBER OF SEQ ID NOS: 31
 20 <170> SOFTWARE: PatentIn version 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 2602
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Drosophila melanogaster
 27 <400> SEQUENCE: 1

P.6

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132 Leu Leu Cys Leu Pro Val Met Leu Leu Asn Glu Gly Ala Glu Phe Arg
133 35 40 45
136 Cys Met Tyr Leu Leu Leu Val Met Ala Ile Phe Trp Val Thr Glu Ala
137 50 55 60
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141 65 70 75 80
144 Met Gly Ile Met Ser Ser Asp Gln Thr Cys Arg Leu Tyr Phe Lys Asp
145 85 90 95
148 Thr Leu Val Met Phe Met Gly Gly Ile Met Val Ala Leu Ala Val Glu
149 100 105 110
152 Tyr Cys Asn Leu His Lys Arg Leu Ala Leu Arg Val Ile Gln Ile Val
153 115 120 125
156 Gly Cys Ser Pro Arg Arg Leu His Phe Gly Leu Ile Met Val Thr Met
157 130 135 140
160 Phe Leu Ser Met Trp Ile Ser Asn Ala Ala Cys Thr Ala Met Met Cys
161 145 150 155 160
164 Pro Ile Ile Gln Ala Val Leu Glu Glu Leu Gln Ala Gln Gly Val Cys
165 165 170 175
168 Lys Ile Asn His Glu Pro Gln Tyr Gln Ile Val Gly Gly Asn Lys Lys
169 180 185 190
172 Asn Asn Glu Asp Glu Pro Pro Tyr Pro Thr Lys Ile Thr Leu Cys Tyr
173 195 200 205
176 Tyr Leu Gly Ile Ala Tyr Ala Ser Ser Leu Gly Gly Cys Gly Thr Ile

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184 Phe Lys Asn Ser Thr Glu Gln Met Asp Phe Pro Thr Phe Met Phe Tyr
185      245      250      255
188 Ser Val Pro Ser Met Leu Val Tyr Thr Leu Leu Thr Phe Val Phe Leu
189      260      265      270
192 Gln Trp His Phe Met Gly Leu Trp Arg Pro Lys Ser Lys Glu Ala Gln
193      275      280      285
196 Glu Val Gln Arg Gly Arg Glu Gly Ala Asp Val Ala Lys Lys Val Ile
197      290      295      300
200 Asp Gln Arg Tyr Lys Asp Leu Gly Pro Met Ser Ile His Glu Ile Gln
201 305      310      315      320
204 Val Met Ile Leu Phe Ile Phe Met Val Val Met Tyr Phe Thr Arg Lys
205      325      330      335
208 Pro Gly Ile Phe Leu Gly Trp Ala Asp Leu Leu Asn Ser Lys Asp Ile
209      340      345      350
212 Arg Asn Ser Met Pro Thr Ile Phe Val Val Val Met Cys Phe Met Leu
213      355      360      365
216 Pro Ala Asn Tyr Ala Phe Leu Arg Tyr Cys Thr Arg Arg Gly Gly Pro
217      370      375      380
220 Val Pro Thr Gly Pro Thr Pro Ser Leu Ile Thr Trp Lys Phe Ile Gln
221 385      390      395      400
224 Thr Lys Val Pro Trp Gly Leu Val Phe Leu Leu Gly Gly Gly Phe Ala
225      405      410      415
228 Leu Ala Glu Gly Ser Lys Gln Ser Gly Met Ala Lys Leu Ile Gly Asn
229      420      425      430
232 Ala Leu Ile Gly Leu Lys Val Leu Pro Asn Ser Val Leu Leu Val
233      435      440      445
236 Val Ile Leu Val Ala Val Phe Leu Thr Ala Phe Ser Ser Asn Val Ala
237      450      455      460
240 Ile Ala Asn Ile Ile Ile Pro Val Leu Ala Glu Met Ser Leu Ala Ile
241 465      470      475      480
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245      485      490      495
248 Met Ala Phe His Leu Pro Val Ser Thr Pro Pro Asn Ala Leu Val Ala
249      500      505      510
252 Gly Tyr Ala Asn Ile Arg Thr Lys Asp Met Ala Ile Ala Gly Ile Gly
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256 Pro Thr Ile Ile Thr Ile Ile Thr Leu Phe Val Phe Cys Gln Thr Trp
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278 acaagtttgc caggtgtgcc tatgttataa tcctcatggc catctactgg tgcacagatg      180
280 tcatcccagt ggctatcact tccctcctgc ctgtcttact cttcccactt ttgaagggttc      240
282 tggactccaa gcaggatatgt gtccaatata tgacggacac caacatgctg ttcctgggca      300
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286 tgctactctt tgtggggacc aagccttcac ggctgatgct gggcttcatt ttcgtcacag      420
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401 35 40 45
404 Trp Cys Thr Asp Val Ile Pro Val Ala Ile Thr Ser Leu Leu Pro Val
405 50 55 60
408 Leu Leu Phe Pro Leu Leu Lys Val Leu Asp Ser Lys Gln Val Cys Val
409 65 70 75 80
412 Gln Tyr Met Thr Asp Thr Asn Met Leu Phe Leu Gly Ser Leu Ile Val
413 85 90 95
416 Ala Thr Ala Val Glu Arg Trp Glu Leu His Lys Arg Ile Ala Leu Arg
417 100 105 110
420 Met Leu Leu Phe Val Gly Thr Lys Pro Ser Arg Leu Met Leu Gly Phe
421 115 120 125
424 Met Phe Val Thr Ala Phe Leu Ser Met Trp Ile Ser Asn Thr Ala Thr
425 130 135 140
428 Thr Ala Met Met Ile Pro Ile Val Glu Ala Met Leu Glu Gln Met Val
429 145 150 155 160
432 Ala Thr Asn Val Ala Val Asp Ala Ser Gln Arg Thr Met Glu Leu Leu
433 165 170 175
436 Asp Lys Asn Lys Ala Ser Glu Leu Pro Gly Ser Gln Val Val Phe Glu
437 180 185 190
440 Asp Pro Ser Val Gln Lys Gln Glu Asp Glu Glu Thr Lys Asn Met Tyr
441 195 200 205
444 Lys Ala Met Asn Leu Cys Val Cys Tyr Ala Ala Ser Ile Gly Gly Thr
445 210 215 220
448 Ala Thr Leu Thr Gly Thr Gly Pro Asn Val Val Leu Leu Gly Gln Met
449 225 230 235 240
452 Gln Glu Leu Phe Pro Asp Ser Lys Asp Val Met Asn Phe Ala Ser Trp
453 245 250 255
456 Phe Ala Phe Ala Leu Pro Asn Met Leu Leu Met Leu Val Met Ala Trp
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460 Leu Trp Leu Leu Cys Phe Tyr Met Arg Pro Asn Leu Lys Lys Thr Cys
461 275 280 285
464 Ile Cys Cys Gly Arg Lys Lys Lys Asp Thr Glu Lys Ile Ala Ser Lys

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:29; Xaa Pos. 1,3,4,6,7,9,10,11,12,13,15,16

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:15,16,17,18,19,20,21,22,23,24,25,26,27,28,29

VERIFICATION SUMMARY

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